

SEQUENCE LISTING

<110> C. Frank Bennett
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION

<130> RTS-0147

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<213> Homo sapiens

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<221> CDS

<222> (257)...(1213)

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acttctgaga aggttgcgca cagctgtgcc cggcagtcta gaggcgcaga agaggaagcc	180
atcgctggc cccggctctc tggaccttgt ctgcctcggg agcggaaaca gcggcagcca	240
gagaactggt ttaatc atg gac aaa caa aac tca cag atg aat gct tct cac	292
Met Asp Lys Gln Asn Ser Gln Met Asn Ala Ser His	
1 5 10	
ccg gaa aca aac ttg cca gtt ggg tat cct cct cag tat cca ccg aca	340
Pro Glu Thr Asn Leu Pro Val Gly Tyr Pro Pro Gln Tyr Pro Pro Thr	
15 20 25	
gca ttc caa gga cct cca gga tat agt ggc tac cct ggg ccc cag gtc	388
Ala Phe Gln Gly Pro Pro Gly Tyr Ser Gly Tyr Pro Gly Pro Gln Val	
30 35 40	
agc tac cca ccc cca cca gcc ggc cat tca ggt cct ggc cca gct ggc	436
Ser Tyr Pro Pro Pro Pro Ala Gly His Ser Gly Pro Gly Pro Ala Gly	
45 50 55 60	
ttt cct gtc cca aat cag cca gtg tat aat cag cca gta tat aat cag	484
Phe Pro Val Pro Asn Gln Pro Val Tyr Asn Gln Pro Val Tyr Asn Gln	
65 70 75	
cca gtt gga gct gca ggg gta cca tgg atg cca gcg cca cag cct cca	532
Pro Val Gly Ala Ala Gly Val Pro Trp Met Pro Ala Pro Gln Pro Pro	
80 85 90	
tta aac tgt cca cct gga tta gaa tat tta agt cag ata gat cag ata	580
Leu Asn Cys Pro Pro Gly Leu Glu Tyr Leu Ser Gln Ile Asp Gln Ile	

95	100	105		
ctg att cat cag caa att gaa ctt ctg gaa gtt tta aca ggt ttt gaa			628	
Leu Ile His Gln Gln Ile Glu Leu Leu Glu Val Leu Thr Gly Phe Glu				
110	115	120		
act aat aac aaa tat gaa att aag aac agc ttt gga cag agg gtt tac			676	
Thr Asn Asn Lys Tyr Glu Ile Lys Asn Ser Phe Gly Gln Arg Val Tyr				
125	130	135	140	
ttt gca gcg gaa gat act gat tgc tgt acc cga aat tgc tgt ggg cca			724	
Phe Ala Ala Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Gly Pro				
	145	150	155	
tct aga cct ttt acc ttg agg att att gat aat atg ggt caa gaa gtc			772	
Ser Arg Pro Phe Thr Leu Arg Ile Ile Asp Asn Met Gly Gln Glu Val				
	160	165	170	
ata act ctg gag aga cca cta aga tgt agc agc tgt tgt tgt ccc tgc			820	
Ile Thr Leu Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Cys Pro Cys				
	175	180	185	
tgc ctt cag gag ata gaa atc caa gct cct cct ggt gta cca ata ggt			868	
Cys Leu Gln Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly				
	190	195	200	
tat gtt att cag act tgg cac cca tgt cta cca aag ttt aca att caa			916	
Tyr Val Ile Gln Thr Trp His Pro Cys Leu Pro Lys Phe Thr Ile Gln				
	205	210	215	220
aat gag aaa aga gag gat gta cta aaa ata agt ggt cca tgt gtt gtg			964	
Asn Glu Lys Arg Glu Asp Val Leu Lys Ile Ser Gly Pro Cys Val Val				
	225	230	235	
tgc agc tgt tgt gga gat gtt gat ttt gag att aaa tct ctt gat gaa			1012	
Cys Ser Cys Cys Gly Asp Val Asp Phe Glu Ile Lys Ser Leu Asp Glu				
	240	245	250	
cag tgt gtg gtt ggc aaa att tcc aag cac tgg act gga att ttg aga			1060	
Gln Cys Val Val Gly Lys Ile Ser Lys His Trp Thr Gly Ile Leu Arg				
	255	260	265	
gag gca ttt aca gac gct gat aac ttt gga atc cag ttc cct tta gac			1108	
Glu Ala Phe Thr Asp Ala Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp				

270 275 280

ctt gat gtt aaa atg aaa gct gta atg att ggt gcc tgt ttc ctc att 1156
Leu Asp Val Lys Met Lys Ala Val Met Ile Gly Ala Cys Phe Leu Ile
285 290 295 300

gac ttc atg ttt ttt gaa agc act ggc agc cag gaa caa aaa tca gga 1204
Asp Phe Met Phe Phe Glu Ser Thr Gly Ser Gln Glu Gln Lys Ser Gly
305 310 315

gtg tgg tag tggattagt aaagtctcct caggaaatct gaagtctgta tattgattga 1263
Val Trp

gactatctaa actcatacct gtatgaatta agctgtaagg cctgtagctc tggttgtata 1323

cttttgcttt tcaaattata gtttatcttc tgtataactg atttataaag gtttttgtac 1383

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accaaataatt aactaaggcc ttattaatth ttatataaat tatatcttgt cctattaaat 1563

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caaattattg ttagtaaaga acaaaatgat tctctcccaa agaaagacac attttaaata 1863

ctccttcact ctaaaactct ggtattataa cttttgaaag ttaatatttc tacatgaaat 1923

gttttagctct tacactctat ccttcttaga aaatggtaat tgagattact cagatattaa 1983

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ttactcccag acccttttcc ggctga

26

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gaaggtgaag gtcggagtc

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caagcttccc gttctcagcc

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agtcgctgct ggtgctagga ttctaggaat tcgcctcact tggagctgca tgagaaaaga 180
aaggcttgca a atg gag gct cct cgc tca gga aca tac ttg cca gct ggg 230
Met Glu Ala Pro Arg Ser Gly Thr Tyr Leu Pro Ala Gly
1 5 10
tat gcc cct cag tat cct cca gca gca gtc caa gga cct cca gag cat 278
Tyr Ala Pro Gln Tyr Pro Pro Ala Ala Val Gln Gly Pro Pro Glu His
15 20 25
act gga cgc ccc aca ttc cag act aac tac caa gtt ccc cag tct ggt 326
Thr Gly Arg Pro Thr Phe Gln Thr Asn Tyr Gln Val Pro Gln Ser Gly
30 35 40 45
tat cca gga cct cag gct agc tac aca gtc tca aca tct gga cat gaa 374
Tyr Pro Gly Pro Gln Ala Ser Tyr Thr Val Ser Thr Ser Gly His Glu
50 55 60
ggt tat gct gct aca cgg ctt cct att caa aat aat cag act ata gtc 422
Gly Tyr Ala Ala Thr Arg Leu Pro Ile Gln Asn Asn Gln Thr Ile Val
65 70 75
ctt gca aac act cag tgg atg cca gca cca cca cct att ctg aac tgc 470
Leu Ala Asn Thr Gln Trp Met Pro Ala Pro Pro Pro Ile Leu Asn Cys
80 85 90
cca cct ggg cta gaa tac tta aat cag ata gat cag ctt ctg att cat 518
Pro Pro Gly Leu Glu Tyr Leu Asn Gln Ile Asp Gln Leu Leu Ile His
95 100 105
cag caa gtt gaa ctt cta gaa gtc tta aca ggc ttt gaa aca aat aac 566
Gln Gln Val Glu Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn
110 115 120 125
aaa ttt gaa atc aag aac agc ctc ggg cag atg gtt tat gtt gca gtg 614
Lys Phe Glu Ile Lys Asn Ser Leu Gly Gln Met Val Tyr Val Ala Val
130 135 140
gaa gat act gac tgc tgt act cga aat tgc tgt gaa gcg tct aga cct 662

Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Glu Ala Ser Arg Pro
 145 150 155

ttc acc tta aga atc ctg gat cat ctg ggc caa gaa gtc atg act ctg 710
 Phe Thr Leu Arg Ile Leu Asp His Leu Gly Gln Glu Val Met Thr Leu
 160 165 170

gag cga cct ctg aga tgc agt agc tgc tgc ttc ccc tgc tgc ctc cag 758
 Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Phe Pro Cys Cys Leu Gln
 175 180 185

gag ata gaa atc cag gct cct ccg ggg gtg cca ata ggt tat gtg act 806
 Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Thr
 190 195 200 205

cag acc tgg cac cca tgt ctg cca aag ctc act ctt cag aac gac aag 854
 Gln Thr Trp His Pro Cys Leu Pro Lys Leu Thr Leu Gln Asn Asp Lys
 210 215 220

agg gag aat gtt cta aaa gta gtt ggt cca tgt gtt gca tgc acc tgc 902
 Arg Glu Asn Val Leu Lys Val Val Gly Pro Cys Val Ala Cys Thr Cys
 225 230 235

tgt tca gat att gac ttt gag atc aag tct ctt gat gaa gtg act aga 950
 Cys Ser Asp Ile Asp Phe Glu Ile Lys Ser Leu Asp Glu Val Thr Arg
 240 245 250

att ggt aag atc acc aag cag tgg tct ggt tgt gtg aaa gag gcc ttc 998
 Ile Gly Lys Ile Thr Lys Gln Trp Ser Gly Cys Val Lys Glu Ala Phe
 255 260 265

acg gat tcg gat aac ttt ggg atc caa ttc ccg cta gac ctg gag gtg 1046
 Thr Asp Ser Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Glu Val
 270 275 280 285

aag atg aaa gct gtg acg ctt ggt gct tgc ttc ctc ata gat tac atg 1094
 Lys Met Lys Ala Val Thr Leu Gly Ala Cys Phe Leu Ile Asp Tyr Met
 290 295 300

ttt ttt gaa ggc tgt gag tag gaacagaaat ccgacctgca gtaggaatca 1145
 Phe Phe Glu Gly Cys Glu
 305

atgaaagagg acagagaaga tctgaagtct acacaaggag atcatatgat tgagagacct 1205

ggggcttttt gatttcttca ttgaaatttc tcagaatcaa gctgttatac atgaagcata 1265
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<400> 13

agcagcgact cagctctcca gactcct

27

<210> 14

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<213> Artificial Sequence

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ttaaactgtc cacctggatt agaatatatta agtcaggtaa tttcaaagac aaaaaatact 180

cataaaaaac agaactgtgc ttccagcttg cttaaccaga ttagcaaagc aataattcac 240

caaagtctga aatagcaaaa ctgtatttcc tgctaacaga ttactctaatt tcttctaggt 300

ctggttcaat tttaaagcaa aatacaaagc ccttagaaaa ttgtattttc tggtatctta 360

aatacaatct atgataatgg ccaatagcaa acatttaatt agcaactgttt cctgcctttg 420

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ctatattaat ataaaataga aattgttaaa tatttcagga aaactttctg aaatataatt 180
tctccgtaca atgaaacagt ttttttcata tatctataaa tagatacagg agcctccagt 240
tatctaata gaagttacata tgggtgcataa ttttaataacc atatttgttt catcttactt 300
caaatttgaa agtacttttg ctataagttt cctaaaagta tttaataactt ttttttttca 360
atttagatta aantcttgat gaacagtgtg tgggtggcaa aattncaagc actggctgga 420
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gacttcatgt tttttgaaag ccctggcagc caggaacaaa aatcaggagt gtggtagtgg 180
attagtgaag gtctctcag gaaatctgaa gtctgtatat tgattgagac tatctaaact 240
catacctgta tgaattaagc tgtaaggcct gtagctctgg ttgtatactt ttgcttttca 300
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tcctttttccc ggttccccgc

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<210> 24
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Thr Tyr Leu Pro Ala Gly Tyr Ala Pro Gln Tyr Pro Pro Ala Ala Val
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Gln Gly Pro Pro Glu His Thr Gly Arg Pro Thr Phe Gln Thr Asn Tyr
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Gln Val Pro Gln Ser Gly Tyr Pro Gly Pro Gln Ala Ser Tyr Thr Val
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Ser Thr Ser Gly His Glu Gly Tyr Ala Ala Thr Arg Leu Pro Ile Gln
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